

SEQUENCE LISTING

SEQ ID NO.1

SEQUENCE LENGTH: 556

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION

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Met Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg
 1           5           10           15
Ser Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His Phe Thr
          20           25           30
Asp Val Phe Ile Ala Gly Ser Gly Pro Ile Ser Cys Thr Tyr Ala Arg
          35           40           45
His Ile Ile Asp Asn Thr Ser Thr Thr Lys Val Tyr Met Ala Glu Ile
          50           55           60
Gly Ser Gln Asp Asn Pro Val Ile Gly Ala His His Lys Asn Ser Ile
 65           70           75           80
Lys Phe Gln Lys Asp Ile Asp Lys Phe Val Asn Ile Ile Asn Gly Ala
          85           90           95
Leu Gln Pro Ile Ser Ile Ser Pro Ser Asp Thr Tyr Gln Pro Thr Leu
          100          105          110
Ala Val Ala Ala Trp Ala Pro Pro Ile Asp Pro Ala Glu Gly Gln Leu
          115          120          125
Val Ile Met Gly His Asn Pro Asn Gln Glu Ala Gly Leu Asn Leu Pro
          130          135          140
Gly Ser Ala Val Thr Arg Thr Val Gly Gly Met Ala Thr His Trp Thr
145           150           155           160
Cys Ala Cys Pro Thr Pro His Asp Glu Glu Arg Val Asn Asn Pro Val
          165          170          175
Asp Lys Gln Glu Phe Asp Ala Leu Leu Glu Arg Ala Lys Thr Leu Leu
          180          185          190
Asn Val His Ser Asp Gln Tyr Asp Asp Ser Ile Arg Gln Ile Val Val
          195          200          205
Lys Glu Thr Leu Gln Gln Thr Leu Asp Ala Ser Arg Gly Val Thr Thr
          210          215          220

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Leu Pro Leu Gly Val Glu Arg Arg Thr Asp Asn Pro Ile Tyr Val Thr
 225 230 235 240
 Trp Thr Gly Ala Asp Thr Val Leu Gly Asp Val Pro Lys Ser Pro Arg
 245 250 255
 Phe Ala Leu Val Thr Glu Thr Arg Val Thr Lys Leu Ile Val Ser Glu
 260 265 270
 Thr Asn Pro Thr Gln Val Val Ala Ala Leu Leu Arg Asn Leu Asn Thr
 275 280 285
 Ser Asn Asp Glu Leu Val Val Ala Lys Ser Phe Val Ile Ala Cys Gly
 290 295 300
 Ala Val Cys Thr Pro Gln Ile Leu Trp Asn Ser Asn Ile Arg Pro Tyr
 305 310 315 320
 Ala Leu Gly Arg Tyr Leu Ser Glu Gln Ser Met Thr Phe Cys Gln Ile
 325 330 335
 Val Leu Lys Arg Gly Ile Val Asp Ala Ile Ala Thr Asp Pro Arg Phe
 340 345 350
 Ala Ala Lys Val Glu Ala His Lys Lys Lys His Pro Asp Asp Val Leu
 355 360 365
 Pro Ile Pro Phe His Glu Pro Glu Pro Gln Val Met Ile Pro Tyr Thr
 370 375 380
 Ser Asp Phe Pro Trp His Val Gln Val His Arg Asp Ala Phe Ser Tyr
 385 390 395 400
 Gly Asp Val Gly Pro Lys Ala Asp Pro Arg Val Val Val Asp Leu Arg
 405 410 415
 Phe Phe Gly Lys Ser Asp Ile Val Glu Glu Asn Arg Val Thr Phe Gly
 420 425 430
 Pro Asn Pro Lys Leu Arg Glu Trp Glu Ala Gly Val Thr Asp Thr Tyr
 435 440 445
 Gly Met Pro Gln Pro Thr Phe His Val Lys Arg Thr Asn Ala Asp Gly
 450 455 460
 Asp Arg Asp Gln Arg Met Met Asn Asp Met Thr Asn Val Ala Asn Met
 465 470 475 480
 Leu Gly Gly Tyr Leu Pro Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly
 485 490 495
 Leu Val Leu His Ile Thr Gly Thr Thr Arg Ile Gly Thr Asp Asp Gln
 500 505 510

Thr Ser Val Ala Asp Pro Thr Ser Lys Val His Asn Phe Asn Asn Leu
 515 520 525
 Trp Val Gly Gly Asn Gly Cys Ile Pro Asp Ala Thr Ala Cys Asn Pro
 530 535 540
 Thr Arg Thr Ser Val Ala Tyr Ala Leu Lys Gly Ala Glu Ala Val Val
 545 550 555 560
 Asn Tyr Leu Gly Val Ser *
 565

SEQ ID NO.2

SEQUENCE LENGTH: 1701

SEQUENCE TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to RNA

SEQUENCE DESCRIPTION

ATG CCG ATA CGT CTT TCC AAA GAA AAA ATC AAC GAC CTG CTG CAA CGT	48
Met Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg	
1 5 10 15	
TCT CAA GGG GAT CTT ACT TCC TCG CAA CAC GAA ATT GTA CAT TTC ACT	96
Ser Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His Phe Thr	
20 25 30	
GAT GTT TTC ATT GCT GGC AGT GGT CCC ATT AGC TGT ACT TAC GCC CGC	144
Asp Val Phe Ile Ala Gly Ser Gly Pro Ile Ser Cys Thr Tyr Ala Arg	
35 40 45	
CAC ATC ATT GAC AAT ACC TCA ACT ACA AAG GTT TAC ATG GCC GAA ATA	192
His Ile Ile Asp Asn Thr Ser Thr Thr Lys Val Tyr Met Ala Glu Ile	
50 55 60	
GGT TCT CAA GAT AAC CCT GTC ATC GGG GCC CAT CAC AAG AAC TCC ATA	240
Gly Ser Gln Asp Asn Pro Val Ile Gly Ala His His Lys Asn Ser Ile	
65 70 75 80	
AAG TTT CAG AAA GAC ATT GAC AAG TTT GTG AAT ATC ATC AAC GGT GCC	288
Lys Phe Gln Lys Asp Ile Asp Lys Phe Val Asn Ile Ile Asn Gly Ala	
85 90 95	

CTC	CAG	CCG	ATT	TCG	ATT	TCG	CCA	TCG	GAC	ACC	TAC	CAG	CCC	ACT	CTC	336
Leu	Gln	Pro	Ile	Ser	Ile	Ser	Pro	Ser	Asp	Thr	Tyr	Gln	Pro	Thr	Leu	
			100					105					110			
GCT	GTA	GCA	GCG	TGG	GCG	CCG	CCC	ATC	GAT	CCT	GCC	GAA	GGC	CAG	CTC	384
Ala	Val	Ala	Ala	Trp	Ala	Pro	Pro	Ile	Asp	Pro	Ala	Glu	Gly	Gln	Leu	
			115					120					125			
GTG	ATT	ATG	GGA	CAC	AAT	CCG	AAT	CAG	GAG	GCC	GGC	CTG	AAC	CTT	CCC	432
Val	Ile	Met	Gly	His	Asn	Pro	Asn	Gln	Glu	Ala	Gly	Leu	Asn	Leu	Pro	
			130				135						140			
GGT	AGC	GCT	GTC	ACT	AGG	ACA	GTC	GGG	GGG	ATG	GCG	ACC	CAC	TGG	ACT	480
Gly	Ser	Ala	Val	Thr	Arg	Thr	Val	Gly	Gly	Met	Ala	Thr	His	Trp	Thr	
			145				150				155				160	
TGC	GCG	TGT	CCT	ACT	CCA	CAT	GAC	GAA	GAG	AGG	GTC	AAC	AAC	CCA	GTT	528
Cys	Ala	Cys	Pro	Thr	Pro	His	Asp	Glu	Glu	Arg	Val	Asn	Asn	Pro	Val	
							165				170				175	
GAC	AAG	CAG	GAG	TTC	GAC	GCA	CTG	CTC	GAA	CGT	GCT	AAA	ACA	TTG	CTC	576
Asp	Lys	Gln	Glu	Phe	Asp	Ala	Leu	Leu	Glu	Arg	Ala	Lys	Thr	Leu	Leu	
			180					185					190			
AAC	GTT	CAC	AGC	GAC	CAG	TAC	GAC	GAT	TCT	ATC	CGT	CAG	ATA	GTT	GTC	624
Asn	Val	His	Ser	Asp	Gln	Tyr	Asp	Asp	Ser	Ile	Arg	Gln	Ile	Val	Val	
			195					200					205			
AAA	GAG	ACT	CTT	CAG	CAG	ACC	CTT	GAT	GCG	TCG	CGG	GGT	GTG	ACC	ACT	672
Lys	Glu	Thr	Leu	Gln	Gln	Thr	Leu	Asp	Ala	Ser	Arg	Gly	Val	Thr	Thr	
			210				215					220				
CTC	CCG	CTG	GGG	GTG	GAG	CGC	CGT	ACG	GAC	AAT	CCT	ATT	TAT	GTC	ACC	720
Leu	Pro	Leu	Gly	Val	Glu	Arg	Arg	Thr	Asp	Asn	Pro	Ile	Tyr	Val	Thr	
			225				230				235				240	
TGG	ACC	GGT	GCC	GAT	ACC	GTC	CTT	GGT	GAT	GTG	CCG	AAG	AGT	CCC	CGA	768
Trp	Thr	Gly	Ala	Asp	Thr	Val	Leu	Gly	Asp	Val	Pro	Lys	Ser	Pro	Arg	
							245			250				255		
TTC	GCT	TTG	GTT	ACA	GAG	ACG	AGA	GTG	ACG	AAG	CTT	ATT	GTC	AGT	GAA	816
Phe	Ala	Leu	Val	Thr	Glu	Thr	Arg	Val	Thr	Lys	Leu	Ile	Val	Ser	Glu	
			260					265					270			
ACC	AAT	CCG	ACG	CAG	GTT	GTT	GCT	GCG	TTG	CTA	CGT	AAC	TTG	AAT	ACA	864
Thr	Asn	Pro	Thr	Gln	Val	Val	Ala	Ala	Leu	Leu	Arg	Asn	Leu	Asn	Thr	
			275					280					285			

AGC	AAC	GAT	GAA	CTT	GTC	GTG	GCC	AAG	AGT	TTC	GTC	ATA	GCT	TGT	GGA	912
Ser	Asn	Asp	Glu	Leu	Val	Val	Ala	Lys	Ser	Phe	Val	Ile	Ala	Cys	Gly	
290							295					300				
GCA	GTC	TGC	ACA	CCG	CAA	ATC	TTG	TGG	AAC	AGC	AAC	ATC	CGC	CCA	TAT	960
Ala	Val	Cys	Thr	Pro	Gln	Ile	Leu	Trp	Asn	Ser	Asn	Ile	Arg	Pro	Tyr	
305						310				315					320	
GCG	CTT	GGT	CGC	TAC	CTC	AGC	GAA	CAG	TCC	ATG	ACT	TTT	TGT	CAG	ATC	1008
Ala	Leu	Gly	Arg	Tyr	Leu	Ser	Glu	Gln	Ser	Met	Thr	Phe	Cys	Gln	Ile	
				325					330					335		
GTT	CTC	AAG	AGG	GGC	ATA	GTC	GAT	GCC	ATC	GCT	ACT	GAC	CCT	CGC	TTC	1056
Val	Leu	Lys	Arg	Gly	Ile	Val	Asp	Ala	Ile	Ala	Thr	Asp	Pro	Arg	Phe	
			340					345					350			
GCT	GCG	AAG	GTT	GAG	GCG	CAC	AAG	AAG	AAG	CAC	CCC	GAT	GAC	GTG	CTG	1104
Ala	Ala	Lys	Val	Glu	Ala	His	Lys	Lys	Lys	His	Pro	Asp	Asp	Val	Leu	
		355					360					365				
CCC	ATT	CCA	TTC	CAC	GAG	CCT	GAA	CCT	CAA	GTG	ATG	ATT	CCG	TAC	ACG	1152
Pro	Ile	Pro	Phe	His	Glu	Pro	Glu	Pro	Gln	Val	Met	Ile	Pro	Tyr	Thr	
	370					375					380					
TCG	GAC	TTC	CCT	TGG	CAT	GTT	CAG	GTG	CAT	CGC	GAT	GCA	TTC	TCA	TAT	1200
Ser	Asp	Phe	Pro	Trp	His	Val	Gln	Val	His	Arg	Asp	Ala	Phe	Ser	Tyr	
385					390				395						400	
GGT	GAT	GTT	GGA	CCC	AAG	GCC	GAC	CCG	CGT	GTT	GTC	GTC	GAT	CTG	AGG	1248
Gly	Asp	Val	Gly	Pro	Lys	Ala	Asp	Pro	Arg	Val	Val	Val	Asp	Leu	Arg	
			405					410					415			
TTT	TTC	GGC	AAA	TCA	GAT	ATT	GTC	GAA	GAA	AAT	CGA	GTG	ACT	TTC	GGT	1296
Phe	Phe	Gly	Lys	Ser	Asp	Ile	Val	Glu	Glu	Asn	Arg	Val	Thr	Phe	Gly	
		420					425					430				
CCG	AAC	CCT	AAG	CTA	CGC	GAG	TGG	GAA	GCG	GGT	GTT	ACA	GAC	ACT	TAT	1344
Pro	Asn	Pro	Lys	Leu	Arg	Glu	Trp	Glu	Ala	Gly	Val	Thr	Asp	Thr	Tyr	
	435					440					445					
GGA	ATG	CCA	CAG	CCG	ACA	TTC	CAT	GTC	AAG	CGG	ACC	AAC	GCC	GAT	GGA	1392
Gly	Met	Pro	Gln	Pro	Thr	Phe	His	Val	Lys	Arg	Thr	Asn	Ala	Asp	Gly	
	450					455				460						
GAC	CGT	GAC	CAG	AGG	ATG	ATG	AAT	GAT	ATG	ACC	AAC	GTC	GCG	AAC	ATG	1440
Asp	Arg	Asp	Gln	Arg	Met	Met	Asn	Asp	Met	Thr	Asn	Val	Ala	Asn	Met	
465				470				475				480				

CTG GGT GGG TAC CTT CCT GGC TCC TAC CCT CAA TTT ATG GCA CCT GGT	1488
Leu Gly Gly Tyr Leu Pro Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly	
485 490 495	
CTC GTA CTG CAC ATC ACG GGA ACT ACT CGG ATC GGG ACA GAT GAT CAA	1536
Leu Val Leu His Ile Thr Gly Thr Thr Arg Ile Gly Thr Asp Asp Gln	
500 505 510	
ACT TCT GTT GCT GAT CCG ACA TCA AAG GTT CAT AAC TTC AAC AAT CTG	1584
Thr Ser Val Ala Asp Pro Thr Ser Lys Val His Asn Phe Asn Asn Leu	
515 520 525	
TGG GTC GGC GGG AAT GGC TGC ATT CCA GAT GCG ACT GCC TGC AAC CCG	1632
Trp Val Gly Gly Asn Gly Cys Ile Pro Asp Ala Thr Ala Cys Asn Pro	
530 535 540	
ACT CGT ACG AGC GTC GCG TAT GCG CTC AAG GGT GCT GAG GCT GTA GTC	1680
Thr Arg Thr Ser Val Ala Tyr Ala Leu Lys Gly Ala Glu Ala Val Val	
545 550 555 560	
AAT TAC CTT GGC GTC TCC TGA	1701
Asn Tyr Leu Gly Val Ser *	
565	

SEQ ID NO.3

SEQUENCE LENGTH: 29

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg Ser

1

5

10

15

Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His

20

25

SEQUENCE DESCRIPTION

SEQUENCE DESCRIPTION

Val Tyr Met Ala Glu Ile Gly Ser Gln Asp Asn Pro Val Ile Gly Ala
1 5 10 15
His His Lys

SEQ ID NO.6

SEQUENCE LENGTH: 61

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Phe Val Asn Ile Ile Asn Gly Ala Leu Gln Pro Ile Ser Ile Ser Pro
 1 5 10 15
 Ser Asp Thr Tyr Gln Pro Thr Leu Ala Val Ala Ala Trp Ala Pro Pro
 20 25 30
 Ile Asp Pro Ala Glu Gly Gln Leu Val Ile Met Gly His Asn Pro Asn
 35 40 45
 Gln Glu Ala Gly Leu Asn Leu Pro Gly Ser Ala Val Thr
 50 55 60

SEQ ID NO.7

SEQUENCE LENGTH: 29

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Arg Thr Val Gly Gly Met Ala Thr His Trp Thr Cys Ala Cys Pro Thr
 1 5 10 15
 Pro His Asp Glu Glu Arg Val Asn Asn Pro Val Asp Lys
 20 25

SEQ ID NO.8

SEQUENCE LENGTH: 31

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Gln	Glu	Phe	Asp	Ala	Leu	Leu	Glu	Arg	Ala	Lys	Thr	Leu	Leu	Asn	Val
1					5					10				15	
His	Ser	Asp	Gln	Tyr	Asp	Asp	Ser	Ile	Arg	Gln	Ile	Val	Val	Lys	
					20				25					30	

SEQ ID NO.9

SEQUENCE LENGTH: 58

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Glu	Thr	Leu	Gln	Gln	Thr	Leu	Asp	Ala	Ser	Arg	Gly	Val	Thr	Thr	Leu
1					5					10				15	
Pro	Leu	Gly	Val	Glu	Arg	Arg	Thr	Asp	Asn	Pro	Ile	Tyr	Val	Thr	Trp
					20				25					30	
Thr	Gly	Ala	Asp	Thr	Val	Leu	Gly	Asp	Val	Pro	Lys	Ser	Pro	Arg	Phe
					35				40					45	
Ala	Leu	Val	Thr	Glu	Thr	Arg	Val	Thr	Lys						
					50				55						

Leu Ile Val Ser Glu Thr Asn Pro Thr Gln Val Val Ala Ala Leu Leu
1 5 10 15
Arg Asn Leu Asn Thr Ser Asn Asp Glu Leu Val Val Ala Lys
20 25 30

Ser Phe Val Ile Ala Cys Gly Ala Val Cys Thr Pro Gln Ile Leu Trp
 1 5 10 15
 Asn Ser Asn Ile Arg Pro Tyr Ala Leu Gly Arg Tyr Leu Ser Glu Gln
 20 25 30
 Ser Met Thr Phe Cys Gln Ile Val Leu Lys Arg Gly Ile Val Asp Ala
 35 40 45
 Ile Ala Thr Asp Pro Arg Phe Ala Ala Lys
 50 55

SEQUENCE LENGTH: 51

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Val Glu Ala His Lys Lys Lys His Pro Asp Asp Val Leu Pro Ile Pro

1 5 10 15

Phe His Glu Pro Glu Pro Gln Val Met Ile Pro Tyr Thr Ser Asp Phe

20 25 30

Pro Trp His Val Gln Val His Arg Asp Ala Phe Ser Tyr Gly Asp Val

35 40 45

Gly Pro Lys

50

SEQUENCE LENGTH: 30

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Ala Asp Pro Arg Val Val Val Asp Leu Arg Phe Phe Gly Lys Ser Asp

1 5 10 15

Ile Val Glu Glu Asn Arg Val Thr Phe Gly Pro Asn Pro Lys

20 25 30

SEQUENCE LENGTH: 50

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

SEQ ID NO.15

SEQUENCE LENGTH: 35

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

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Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly Leu Val Leu His Ile Thr
  1             5             10             15
Gly Thr Thr Arg Ile Gly Thr Asp Asp Gln Thr Ser Val Ala Asp Pro
      20             25             30
Thr Ser Lys
      35

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Lys

1 5 10

20

SEQ ID NO.19

SEQUENCE LENGTH: 26

SEQUENCE TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

SEQUENCE DESCRIPTION

GAGAGACCAT GGGGTATCGT CTTTCC

26

SEQ ID NO.20

SEQUENCE LENGTH: 27

SEQUENCE TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

SEQUENCE DESCRIPTION

GAGAGAGGAT CCGGAGACGC CAAGGAT

27

"GAGAGAGGAT CCGGAGACGC CAAGGAT"